Amendments to the Claims

This listing of claims will replace all prior versions and listings of claims in the application.

Claims 1-67 (canceled)

Claim 68 (currently amended): A method for selecting a nucleic acid molecule encoding a target epitope of cytotoxic T-lymphocytes, comprising:

(a) contacting mammalian host cells with cytotoxic T-lymphocytes specific for said target epitope under conditions wherein a host cell expressing said target epitope undergoes a lytic event upon contact with said T-lymphocytes; wherein said host cells comprise a library of heterologous nucleic acid molecules, at least one of said heterologous nucleic acid molecules encoding said target epitope, wherein said library is constructed in a vaccinia virus vector which expresses said target epitope in said host cells, wherein said host cells express a defined MHC molecule, and wherein said cytotoxic T-lymphocytes are restricted for said MHC molecule; [[and]]

(b) recovering ~~these~~ the floating host cells which are undergoing ~~undergo or have undergone~~ a lytic event[[.]], and

(c) isolating said vector from said recovered host cells, thereby selecting a nucleic acid molecule which encodes said target epitope.

Claim 69 (canceled)

Claim 70 (currently amended): The method of claim 68, further comprising:

~~(c) isolating said vector from said recovered host cells;~~

(d) transferring said vector to a population of mammalian host cells, wherein said vector expresses said target epitope in said host cells, and wherein said host cells express a defined MHC molecule;

(e) contacting said host cells with cytotoxic T-lymphocytes specific for said target epitope and restricted for said MHC molecule, under conditions wherein a host cell expressing said target epitope will undergo a lytic even upon contact with said T-lymphocytes; ~~and~~

(f) recovering ~~those~~ the floating host cells which are undergoing ~~undergo or have undergone~~ a lytic event[[.]], and

(g) isolating said vector from said recovered host cells, thereby selecting a nucleic acid molecule which encodes said target epitope.

Claims 71-78 (canceled)

Claim 79 (previously presented): The method of claim 68, wherein said vector further comprises a transcriptional control signal in operable association with said heterologous nucleic acid molecules, and wherein said transcriptional control signal functions in a vaccinia virus.

Claim 80 (previously presented): The method of claim 79, wherein said transcriptional control signal comprises a promoter.

Claim 81 (previously presented): The method of claim 80, wherein said promoter is constitutive.

Claim 82 (previously presented): The method of claim 80, wherein said promoter is a vaccinia virus p7.5 promoter.

Claim 83 (previously presented): The method of claim 82, wherein said vector comprises the sequence shown in SEQ ID NO:1.

Claim 84 (previously presented): The method of claim 80, wherein said promoter is a synthetic early/late promoter.

Claim 85 (previously presented): The method of claim 84, wherein said vector comprises the sequence shown in SEQ ID NO:3.

Claim 86 (previously presented): The method of claim 79, wherein said transcriptional control signal comprises a transcriptional termination signal.

Claim 87 (previously presented): The method of claim 79, wherein said vector further comprises a translational control signal associated with said transcriptional control signal.

Claim 88 (previously presented): The method of claim 87, wherein said vector comprises the sequence shown in SEQ ID NO:6.

Claim 89 (previously presented): The method of claim 87, wherein said translational control signal comprises a translation initiation codon operably linked to said heterologous nucleic acid molecules.

Claim 90 (previously presented): The method of claim 89, wherein said translation initiation codon occurs in one of three reading frames.

Claim 91 (previously presented): The method of claim 90, wherein said vector comprises a sequence selected from the group consisting of SEQ ID NO:7, SEQ ID NO:8 and SEQ ID NO:9.

Claim 92 (previously presented): The method of claim 68, wherein said library of heterologous nucleic acid molecules is isolated from a tumor cell, and wherein said target epitope is differentially expressed in said tumor cell relative to a non-tumorigenic counterpart cell.

Claim 93 (previously presented): The method of claim 92, wherein said heterologous nucleic acid molecules are cDNA molecules synthesized from said tumor cell.

Claims 94-97 (canceled)

Claim 98 (previously presented): The method of claim 68, wherein said library is constructed by a method comprising:

(a) cleaving a vaccinia virus genome to produce a first viral fragment and a second viral fragment, wherein said first fragment is nonhomologous with said second fragment;

(b) providing a population of transfer plasmids comprising said heterologous nucleic acid molecules flanked by a 5' flanking region and a 3' flanking region, wherein said 5' flanking region is homologous to said first viral fragment and said 3' flanking region is homologous to said second viral fragment; and wherein said transfer plasmids are capable of homologous recombination with said first and second viral fragments such that a viable virus genome is formed;

(c) introducing said transfer plasmids and said first and second viral fragments into a host cell under conditions wherein a transfer plasmid and said viral fragments undergo in vivo homologous recombination, thereby producing a viable modified virus genome comprising a heterologous nucleic acid molecule; and

(d) recovering said modified virus genome.

Claim 99 (previously presented): The method of claim 98, wherein said virus genome comprises a first recognition site for a first restriction endonuclease and a second recognition site for a second restriction endonuclease; and wherein said first and second viral fragments are produced by digesting said viral genome with said first restriction

endonuclease and said second restriction endonuclease, and isolating said first and second viral fragments.

Claim 100 (previously presented): The method of claim 99, wherein said first and second recognition sites are physically arranged in said genome such that the region extending between said first and second viral fragments is not essential for virus infectivity.

Claims 101-103 (canceled)

Claim 104 (previously presented): The method of claim 98, wherein said transfer plasmids and said first and second viral fragments are introduced into a host cell comprising a helper virus, wherein said host cell is non-permissive for the production of infectious virus particles of said helper virus.

Claim 105 (previously presented): The method of claim 104, wherein said helper virus is an avipoxvirus.

Claim 106 (previously presented): The method of claim 105, wherein said helper virus is a fowlpox virus.

Claim 107 (previously presented): The method of claim 99, wherein said first and second restriction enzyme recognition sites are situated in a thymidine kinase gene.

Claim 108 (previously presented): The method of claim 99, wherein said first and second restriction enzyme recognition sites are situated in a vaccinia virus HindIII J fragment.

Claim 109 (canceled)

Claim 110 (previously presented): The method of claim 108, wherein said first restriction enzyme is NotI, and wherein said first restriction enzyme recognition site is GCGGCCGC.

Claim 111 (previously presented): The method of claim 108, wherein said second restriction enzyme site is ApaI, and wherein said second restriction enzyme recognition site is GGGCCC.

Claim 112 (previously presented): The method of claim 98, wherein said vaccinia virus genome comprises a modified thymidine kinase (tk) gene which comprises a 7.5k promoter, a unique NotI restriction site, and a unique ApaI restriction site.

Claim 113 (previously presented): The method of claim 98, wherein said vaccinia virus genome comprises a modified thymidine kinase (tk) gene which comprises a synthetic early/late (E/L) promoter, a unique NotI restriction site, and a unique ApaI restriction site.

Claim 114 (previously presented): The method of claim 98, wherein the 5' and 3' flanking regions of said transfer plasmids are capable of homologous recombination with a vaccinia virus thymidine kinase gene.

Claim 115 (previously presented): The method of claim 114, wherein the 5' and 3' flanking regions of said transfer plasmids are capable of homologous recombination with a vaccinia virus HindIII J fragment.

Claim 116 (currently amended): The method of claim 114, wherein said transfer plasmids comprise heterologous nucleic acid molecules ligated into a plasmid selected from the group consisting of:

(a) p7.5/ATG0/tk, which comprises SEQ ID NO:6;

(b) p7.5/ATG1/tk, which comprises SEQ ID NO:7;

(c) p/7.5/ATG2/tk, which comprises SEQ ID NO:8; and

(d) p7.5/ATG3/tk, which comprises SEQ ID NO:9.

Claim 117 (currently amended): The method of claim 68, wherein said host cells are a monolayer, and wherein ~~those~~ the floating host cells which are undergoing ~~undergo or have undergone~~ a lytic event are released from said monolayer.

Claim 118 (previously presented): The method of claim 68, wherein said MHC molecule is a class I MHC molecule.

Claim 119 (currently amended): The method of claim 70, wherein said host cells are a monolayer, and wherein ~~those~~ the floating host cells which are undergoing ~~undergo or have undergone~~ a lytic event are released from said monolayer.

Claim 120 (previously presented): The method of claim 70, wherein said MHC molecule is a class I MHC molecule.

Claim 121-129 (canceled)